

62. (New) A method of modifying the endogenous oil of a cotton plant comprising the step of introducing into a cotton plant a gene construct which comprises a nucleotide sequence of at least 20 nucleotides of a fatty acid Δ 12-desaturase gene operably in connection with a promoter sequence capable of conferring expression of said nucleotide sequence in the seed of a cotton plant, wherein expression of said nucleotide sequence modifies fatty acid Δ 12-desaturase activity in the seed of the cotton plant.
63. (New) The method according to claim 62 wherein the fatty acid Δ 12-desaturase gene comprises a nucleotide sequence selected from the group consisting of:
- (a) the nucleotide sequence set forth in SEQ ID NO: 3 or SEQ ID NO: 5 or SEQ ID NO: 7; and
- (b) a nucleotide sequence which encodes the amino acid sequence set forth in SEQ ID NO: 4 OR SEQ ID NO: 6.
64. (New) The method according to claim 62 wherein the gene construct comprises an inverted repeat sequence comprising a sequence of at least 25 nucleotides of said fatty acid Δ 12-desaturase gene linked to a nucleotide sequence which is complementary to said sequence of at least 25 nucleotides.
65. (New) The method according to claim 64 wherein the gene construct comprises an inverted repeat sequence comprising a sequence of at least 25 nucleotides from the 5'-untranslated region of SEQ ID NO: 3 or SEQ ID NO: 5 linked to a nucleotide sequence which is complementary to said sequence of at least 25 nucleotides.
66. (New) The method according to claim 64 wherein the gene construct comprises an inverted repeat sequence comprising a sequence of at least 25 nucleotides from the 5'-untranslated region of the *ghFAD2-1* gene set forth in SEQ ID NO: 7 linked to a nucleotide sequence which is complementary to said sequence of at least 25 nucleotides.
67. (New) The method according to claim 62 wherein the gene construct comprises at least 20 nucleotides of the coding region of the nucleotide sequence set forth in SEQ ID NO: 3 or SEQ ID NO: 5, in the antisense orientation.

68. (New) The method according to claim 62, wherein the promoter is the soybean lectin promoter sequence or the *ghFAD2-1* gene promoter.
69. (New) The method according to claim 62 wherein the gene construct is expressed in the cotton seed so as to reduce the level of expression of an endogenous fatty acid $\Delta 12$ -desaturase gene to a level that is sufficient to modify the content and/or composition of the oil produced in said seed.
70. (New) A transgenic cotton plant produced by the method according to claim 62 and having a modified level of fatty acid $\Delta 12$ -desaturase in the seed compared to an isogenic non-transformed plant.
71. (New) A progeny plant of the transgenic cotton plant according to claim 70, wherein said progeny plant comprises the introduced gene construct.
72. (New) The progeny plant according to claim 71 having a modified level of fatty acid $\Delta 12$ -desaturase in the seed compared to an isogenic non-transformed plant.
73. (New) A seed of the transgenic cotton plant according to claim 70 or the progeny plant according to claim 71, comprising the introduced gene construct.
74. (New) A method of modifying the endogenous oil of a cotton plant comprising the steps of:
- (a) producing a transgenic cotton plant by introducing into a cotton plant a gene construct which comprises a nucleotide sequence of at least 20 nucleotides of a fatty acid $\Delta 12$ -desaturase gene operably in connection with a promoter sequence capable of conferring expression of said nucleotide sequence in the seed of a cotton plant; and
 - (b) growing said transgenic plant for a time and under conditions sufficient for the expression of an endogenous fatty acid $\Delta 12$ -desaturase gene to be reduced in the seed by virtue of the presence of the introduced gene construct.
75. (New) The method according to claim 74 wherein the fatty acid $\Delta 12$ -desaturase gene comprises a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence set forth in SEQ ID NO: 3 or SEQ ID NO: 5 or SEQ ID NO: 7;
and
- (b) a nucleotide sequence which encodes the amino acid sequence set forth in SEQ ID NO: 4 or SEQ ID NO: 6.

76. (New) The method according to claim 74, wherein the gene construct comprises an inverted repeat sequence comprising a sequence of at least 25 nucleotides of said fatty acid Δ 12-desaturase gene linked to a nucleotide sequence which is complementary to said sequence of at least 25 nucleotides.

77. (New) The method according to claim 74 wherein the gene construct comprises an inverted repeat sequence comprising a sequence of at least 25 nucleotides from the 5'-untranslated region of SEQ ID NO: 3 or SEQ ID NO: 5 linked to a nucleotide sequence which is complementary to said sequence of at least 25 nucleotides.

78. (New) The method according to claim 74 wherein the gene construct comprises an inverted repeat sequence comprising a sequence of at least 25 nucleotides from the 5'-untranslated region of the *ghFAD2-1* gene set forth in SEQ ID NO: 7 linked to a nucleotide sequence which is complementary to said sequence of at least 25 nucleotides.

79. (New) The method according to claim 74 wherein the gene construct comprises at least 20 nucleotides of the coding region of the nucleotide sequence set forth in SEQ ID NO: 3 or SEQ ID NO: 5, in the antisense orientation.

80. (New) A transgenic cotton plant produced by the method according to claim 74, wherein said transgenic cotton plant has an increased level of oleic acid in its seed compared to a seed of an isogenic non-transformed plant.

81. (New) The transgenic cotton plant of claim 80, wherein said transgenic cotton plant has a reduced level of palmitic acid in its seed compared to a seed of an isogenic non-transformed plant.

82. (New) A progeny plant of the transgenic cotton plant according to claim 80, wherein said progeny plant has an increased level of oleic acid in its seed.
83. (New) A progeny plant of the transgenic cotton plant according to claim 81, wherein said progeny plant has a decreased level of palmitic acid in its seed.
84. (New) A seed of the transgenic cotton plant according to claim 80 or the progeny plant according to claim 82, having said increased level of oleic acid.
85. (New) A seed of the transgenic cotton plant according to claim 81 or the progeny plant according to claim 83, having said decreased level of palmitic acid.
86. (New) The method according to claim 74 further comprising the step of producing a second transgenic cotton plant by introducing into the transgenic cotton plant or a cell of said plant a second gene construct which comprises a nucleotide sequence of at least 20 nucleotides of a fatty acid $\Delta 9$ -desaturase gene operably in connection with a promoter sequence capable of conferring expression of said nucleotide sequence in the seed of a cotton plant, and growing said second transgenic plant for a time and under conditions sufficient to decrease the expression of an endogenous fatty acid $\Delta 9$ -desaturase gene in the seed of said second transgenic cotton plant.
87. (New) The method according to claim 74 wherein said second gene construct is introduced by transformation.
88. (New) The method according to claim 74 comprising:
- (a) crossing a first transgenic cotton plant having an introduced gene construct which comprises a nucleotide sequence of at least 20 nucleotides of a fatty acid $\Delta 9$ -desaturase gene operably in connection with a promoter sequence capable of conferring expression of said nucleotide sequence in the seed of a cotton plant, with a second transgenic cotton plant having an introduced gene construct which comprises a nucleotide sequence of at least 20 nucleotides of a fatty acid $\Delta 12$ -desaturase gene operably in connection with a promoter sequence capable of conferring expression of said nucleotide sequence in the seed of a cotton plant; and

(b) selecting the progeny of said crossing, wherein said progeny have modified fatty acid content compared to an isogenic non-transformed cotton plant.

89. (New) A cotton plant produced by the method according to claim 86 or claim 88, and having an increased level of oleic acid in the seed compared to an isogenic non-transformed plant.

90. (New) A seed of the cotton plant according to claim 89, having said increased level of oleic acid.

91. (New) A cotton plant produced by the method according to claim 86 or claim 88 and having a reduced level of palmitic acid in the seed compared to an isogenic non-transformed plant.

92. (New) A seed of the cotton plant according to claim 91, having said reduced level of palmitic acid.

93. (New) A cotton plant produced by the method according to claim 86 or claim 88 and having an increased level of stearic acid in the seed compared to an isogenic non-transformed plant.

94. (New) A seed of the cotton plant according to claim 93, having said increased level of stearic acid.

95. (New) A cotton plant produced by the method according to claim 86 or claim 88 and having increased levels of stearic acid and oleic acid in the seed compared to an isogenic non-transformed plant.

96. (New) A seed of the cotton plant according to claim 95, having said increased level of stearic acid and oleic acid.

97. (New) The method according to claim 88 wherein the transgenic cotton plant at (a) or (b) is a progeny of a primary transformed plant.

98. (New) A cotton plant having increased levels of oleic acid and stearic acid in the seed, wherein said plant is produced by a process comprising sexual hybridisation between a first cotton plant

having increased oleic acid in the seed compared to an isogenic non-transformed cotton plant and a second cotton plant having increased stearic acid in the seed compared to an isogenic non-transformed cotton plant, and wherein said first cotton plant is a transgenic cotton plant according to claim 70.

99. (New) The cotton plant according to claim 98 wherein said plant has decreased palmitic acid in the seed.
100. (New) A seed of the cotton plant according to claim 98, having said increased levels of oleic acid and stearic acid.
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cn⁺ 101. (New) A gene construct for modifying the fatty acid composition of cottonseed oil, comprising a nucleotide sequence of a fatty acid Δ 12-desaturase gene operably in connection with a promoter sequence that is operable in the seed of a cotton plant, wherein said nucleotide sequence is selected from the group consisting of:
- (a) an inverted repeat sequence comprising a sequence of at least 25 nucleotides from the 5'-untranslated region of SEQ ID NO: 3 or SEQ ID NO: 5 linked to a nucleotide sequence which is complementary to said sequence of at least 25 nucleotides; and
 - (b) an inverted repeat sequence comprising a sequence of at least 25 nucleotides from the 5'-untranslated region of the *ghFAD2-1* gene set forth in SEQ ID NO: 7 linked to a nucleotide sequence which is complementary to said sequence of at least 25 nucleotides.
102. (New) The gene construct according to claim 101 wherein the promoter sequence is a soybean lectin gene promoter sequence or the *ghFAD2-1* gene promoter.
103. (New) The method of claim 64, wherein the inverted repeat sequence comprises an intervening sequence between the sequence of at least 25 nucleotides and the sequence complementary thereto.
104. (New) The method of claim 76, wherein the inverted repeat sequence comprises an intervening sequence between the sequence of at least 25 nucleotides and the sequence complementary thereto.